



SEQUENCE LISTING

<110> Potter, Robert  
Rosenthal, Kim

<120> High Fidelity Reverse Transcriptases and Uses Thereof

<130> 0942.5030001/RWE

<140> 09/808,124

<141> 2001-03-15

<150> 60/189,454

<151> 2000-03-15

<160> 6

<170> PatentIn version 3.0

<210> 1

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide template

<400> 1

gagttacagt gtttttggtc cagtctgtag cagtgtgtga atggaag

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<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide primer

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cttccattca cacactgc

18

<210> 3

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide primer

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gaagatcgca ctccagccag c

21

<210> 4

<211> 298

<212> DNA

<213> Artificial Sequence

<220>

<223> lacZ $\alpha$  peptide in M13mp19 from SuperScript II RT and  
SuperScript II H203R T306K F309N

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agcgcaacgc aattaatgtg agttagctca ctcataggc accccaggct ttacacttta 60

tgcttccggc tcgtatgttg tgtggaattg tgagcggata acaatttcac acaggaaaca 120

gctatgacca tgattacgcc aagcttgcac gcctgcaggt cgactctaga ggatccccgg 180

gtaccgagct cgaattcact ggccgtcgtt ttacaacgtc gtgactggga aaaccctggc 240

gttaccacaac ttaatcgctt tgcagcacat ccccttttcg ccagctggcg taatagcg 298

<210> 5

<211> 1575

<212> DNA

<213> Moloney-Murine Leukemia Virus

<220>

<221> CDS

<222> (1) .. (1575)

<400> 5

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Met Thr Leu Asn Ile Glu Asp Glu His Arg Leu His Glu Thr Ser Lys  
1 5 10 15

gag cca gat gtt tct cta ggg tcc aca tgg ctg tct gat ttt cct cag 96  
Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln  
20 25 30

gcc tgg gcg gaa acc ggg ggc atg gga ctg gca gtt cgc caa gct cct 144  
Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro  
35 40 45

ctg atc ata cct ctg aaa gca acc tct acc ccc gtg tcc ata aaa caa 192  
Leu Ile Ile Pro Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln  
50 55 60

tac ccc atg tca caa gaa gcc aga ctg ggg atc aag ccc cac ata cag 240  
Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln  
65 70 75 80

aga ctg ttg gac cag gga ata ctg gta ccc tgc cag tcc ccc tgg aac 288  
Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn  
85 90 95

acg ccc ctg cta ccc gtt aag aaa cca ggg act aat gat tat agg cct 336  
Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro  
100 105 110

gtc cag gat ctg aga gaa gtc aac aag cgg gtg gaa gac atc cac ccc 384  
Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro  
115 120 125

acc gtg ccc aac cct tac aac ctc ttg agc ggg ctc aag cgg gtg gaa 432

Thr	Val	Pro	Asn	Pro	Tyr	Asn	Leu	Leu	Ser	Gly	Leu	Lys	Arg	Val	Glu		
130						135					140						
gac	atc	cac	ccc	acc	gtg	ccc	aac	cct	tac	aac	ctc	ttg	agc	ggg	ctc	480	
Asp	Ile	His	Pro	Thr	Val	Pro	Asn	Pro	Tyr	Asn	Leu	Leu	Ser	Gly	Leu	160	
145					150					155							
cca	ccg	tcc	cac	cag	tgg	tac	act	gtg	ctt	gat	tta	aag	gat	gcc	ttt	528	
Pro	Pro	Ser	His	Gln	Trp	Tyr	Thr	Val	Leu	Asp	Leu	Lys	Asp	Ala	Phe	175	
				165					170								
ttc	tgc	ctg	aga	ctc	cac	ccc	acc	agt	cag	cct	ctc	ttc	gcc	ttt	gag	576	
Phe	Cys	Leu	Arg	Leu	His	Pro	Thr	Ser	Gln	Pro	Leu	Phe	Ala	Phe	Glu	190	
			180					185					190				
tgg	aga	gat	cca	gag	atg	gga	atc	tca	gga	caa	ttg	acc	tgg	acc	aga	624	
Trp	Arg	Asp	Pro	Glu	Met	Gly	Ile	Ser	Gly	Gln	Leu	Thr	Trp	Thr	Arg	205	
		195					200										
ctc	cca	cag	ggg	ttc	aaa	aac	agt	ccc	acc	ctg	ttt	gat	gag	gca	ctg	672	
Leu	Pro	Gln	Gly	Phe	Lys	Asn	Ser	Pro	Thr	Leu	Phe	Asp	Glu	Ala	Leu	220	
		210				215											
cac	aga	gac	cta	gca	gac	ttc	cgg	atc	cag	cac	cca	gac	ttg	atc	ctg	720	
His	Arg	Asp	Leu	Ala	Asp	Phe	Arg	Ile	Gln	His	Pro	Asp	Leu	Ile	Leu	240	
					230					235							
cta	cag	tac	gtg	gat	gac	tta	ctg	ctg	gcc	gcc	act	tct	gag	cta	gac	768	
Leu	Gln	Tyr	Val	Asp	Asp	Leu	Leu	Leu	Ala	Ala	Thr	Ser	Glu	Leu	Asp	255	
				245					250								
tgc	caa	caa	ggg	act	cgg	gcc	ctg	tta	caa	acc	cta	ggg	aac	ctc	ggg	816	
Cys	Gln	Gln	Gly	Thr	Arg	Ala	Leu	Leu	Gln	Thr	Leu	Gly	Asn	Leu	Gly	270	
			260					265					270				
tat	cgg	gcc	tcg	gcc	aag	aaa	gcc	caa	att	tgc	cag	aaa	cag	gtc	aag	864	
Tyr	Arg	Ala	Ser	Ala	Lys	Lys	Ala	Gln	Ile	Cys	Gln	Lys	Gln	Val	Lys	285	
		275					280										
tat	ctg	ggg	tat	ctt	cta	aaa	gag	ggg	cag	aga	tgg	ctg	act	gag	gcc	912	
Tyr	Leu	Gly	Tyr	Leu	Leu	Lys	Glu	Gly	Gln	Arg	Trp	Leu	Thr	Glu	Ala	300	
		290				295											
aga	aaa	gag	act	gtg	atg	ggg	cag	cct	act	ccg	aag	acc	cct	cga	caa	960	
Arg	Lys	Glu	Thr	Val	Met	Gly	Gln	Pro	Thr	Pro	Lys	Thr	Pro	Arg	Gln	320	
		305			310					315							
cta	agg	gag	ttc	cta	ggg	acg	gca	ggc	ttc	tgt	cgc	ctc	tgg	atc	cct	1008	
Leu	Arg	Glu	Phe	Leu	Gly	Thr	Ala	Gly	Phe	Cys	Arg	Leu	Trp	Ile	Pro	335	
				325					330								
ggg	ttt	gca	gaa	atg	gca	gcc	ccc	ttg	tac	cct	ctc	acc	aaa	acg	ggg	1056	
Gly	Phe	Ala	Glu	Met	Ala	Ala	Pro	Leu	Tyr	Pro	Leu	Thr	Lys	Thr	Gly	350	
			340					345									
act	ctg	ttt	aat	tgg	ggc	cca	gac	caa	caa	aag	gcc	tat	caa	gaa	atc	1104	
Thr	Leu	Phe	Asn	Trp	Gly	Pro	Asp	Gln	Gln	Lys	Ala	Tyr	Gln	Glu	Ile		

355	360	365	
aag caa gct ctt cta act gcc cca gcc ctg ggg ttg cca gat ttg act			1152
Lys Gln Ala Leu Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr			
370	375	380	
aag ccc ttt gaa ctc ttt gtc gac gag aag cag ggc tac gcc aaa ggt			1200
Lys Pro Phe Glu Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly			
385	390	395	400
gtc cta acg caa aaa ctg gga cct tgg cgt cgg ccg gtg gcc tac ctg			1248
Val Leu Thr Gln Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu			
	405	410	415
tcc aaa aag cta gac cca gta gca gct ggg tgg ccc cct tgc cta cgg			1296
Ser Lys Lys Leu Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg			
	420	425	430
atg gta gca gcc att gcc gta ctg aca aag gat gca ggc aag cta acc			1344
Met Val Ala Ala Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr			
	435	440	445
atg gga cag cca cta gtc att ctg gcc ccc cat gca gta gag gca cta			1392
Met Gly Gln Pro Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu			
	450	455	460
gtc aaa caa ccc ccc gac cgc tgg ctt tcc aac gcc cgg atg act cac			1440
Val Lys Gln Pro Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His			
	465	470	475
tat cag gcc ttg ctt ttg gac acg gac cgg gtc cag ttc gga ccg gtg			1488
Tyr Gln Ala Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val			
	485	490	495
gta gcc ctg aac ccg gct acg ctg ctc cca ctg cct gag gaa ggg ctg			1536
Val Ala Leu Asn Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu			
	500	505	510
caa cac aac tgc ctt gat aat tcc cgc tta att aat taa			1575
Gln His Asn Cys Leu Asp Asn Ser Arg Leu Ile Asn			
	515	520	

<210> 6

<211> 524

<212> PRT

<213> Moloney-Murine Leukemia Virus

<400> 6

Met	Thr	Leu	Asn	Ile	Glu	Asp	Glu	His	Arg	Leu	His	Glu	Thr	Ser	Lys
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Glu	Pro	Asp	Val	Ser	Leu	Gly	Ser	Thr	Trp	Leu	Ser	Asp	Phe	Pro	Gln			
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Ala	Trp	Ala	Glu	Thr	Gly	Gly	Met	Gly	Leu	Ala	Val	Arg	Gln	Ala	Pro			
		35					40					45						
Leu	Ile	Ile	Pro	Leu	Lys	Ala	Thr	Ser	Thr	Pro	Val	Ser	Ile	Lys	Gln			
	50					55					60							
Tyr	Pro	Met	Ser	Gln	Glu	Ala	Arg	Leu	Gly	Ile	Lys	Pro	His	Ile	Gln			
65					70					75					80			
Arg	Leu	Leu	Asp	Gln	Gly	Ile	Leu	Val	Pro	Cys	Gln	Ser	Pro	Trp	Asn			
				85					90						95			
Thr	Pro	Leu	Leu	Pro	Val	Lys	Lys	Pro	Gly	Thr	Asn	Asp	Tyr	Arg	Pro			
			100					105					110					
Val	Gln	Asp	Leu	Arg	Glu	Val	Asn	Lys	Arg	Val	Glu	Asp	Ile	His	Pro			
		115					120					125						
Thr	Val	Pro	Asn	Pro	Tyr	Asn	Leu	Leu	Ser	Gly	Leu	Lys	Arg	Val	Glu			
	130					135					140							
Asp	Ile	His	Pro	Thr	Val	Pro	Asn	Pro	Tyr	Asn	Leu	Leu	Ser	Gly	Leu			
145					150					155					160			
Pro	Pro	Ser	His	Gln	Trp	Tyr	Thr	Val	Leu	Asp	Leu	Lys	Asp	Ala	Phe			
				165					170					175				
Phe	Cys	Leu	Arg	Leu	His	Pro	Thr	Ser	Gln	Pro	Leu	Phe	Ala	Phe	Glu			
			180					185					190					
Trp	Arg	Asp	Pro	Glu	Met	Gly	Ile	Ser	Gly	Gln	Leu	Thr	Trp	Thr	Arg			
		195					200					205						
Leu	Pro	Gln	Gly	Phe	Lys	Asn	Ser	Pro	Thr	Leu	Phe	Asp	Glu	Ala	Leu			
	210					215					220							
His	Arg	Asp	Leu	Ala	Asp	Phe	Arg	Ile	Gln	His	Pro	Asp	Leu	Ile	Leu			
225					230					235					240			

Leu Gln Tyr Val Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp  
 245 250 255

Cys Gln Gln Gly Thr Arg Ala Leu Leu Gln Thr Leu Gly Asn Leu Gly  
 260 265 270

Tyr Arg Ala Ser Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys  
 275 280 285

Tyr Leu Gly Tyr Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala  
 290 295 300

Arg Lys Glu Thr Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln  
 305 310 315 320

Leu Arg Glu Phe Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro  
 325 330 335

Gly Phe Ala Glu Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly  
 340 345 350

Thr Leu Phe Asn Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile  
 355 360 365

Lys Gln Ala Leu Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr  
 370 375 380

Lys Pro Phe Glu Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly  
 385 390 395 400

Val Leu Thr Gln Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu  
 405 410 415

Ser Lys Lys Leu Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg  
 420 425 430

Met Val Ala Ala Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr  
 435 440 445

Met Gly Gln Pro Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu  
 450 455 460

Val Lys Gln Pro Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His

465

470

475

480

Tyr Gln Ala Leu Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val  
485 490 495

Val Ala Leu Asn Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu  
500 505 510

Gln His Asn Cys Leu Asp Asn Ser Arg Leu Ile Asn  
515 520